

CC-XX	subunit coding sequence	
Sequence 1184	BP; 356 A; 260 C; 235 G; 313 T; 0 U; 0 Other;	
Query Match	100.0%; Score 1184; DB 4; Length 1184;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 1184;	Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 CTTATCCTTATCCAGTATGCACTACGCTCTTGGGTCGCTCATGAGACCCAGGGGCATG	60
DB	1 CTTATCCTTATCCAGTATGCACTACGCTCTTGGGTCGCTCATGAGACCCAGGGGCATG	60
QY	61 TTGGAAGAAGCTGAGAGAAAGAGACAACAAACGGCGAGTGTGTGAGAGAGCAGACGGG	120
DB	61 TTGGAAGAAGCTGAGAGAAAGAGACAACAAACGGCGAGTGTGTGAGAGAGCAGACGGG	120
QY	121 CTGTGGGGCCCTTCCAGAGAAATGTATCTGAAAAAGCTTACGCAATGTCTGGATTGGTA	180
DB	121 CTGTGGGGCCCTTCCAGAGAAATGTATCTGAAAAAGCTTACGCAATGTCTGGATTGGTA	180
QY	181 AACATATCCTGGAAGAAGCAGAGGTTTTTTCATCTCTCCAGAGACATCCACATTAAG	240
DB	181 AACATATCCTGGAAGAAGCAGAGGTTTTTTCATCTCTCCAGAGACATCCACATTAAG	240
QY	241 AAAGGAGACCTGGAACCAACATCTCTTAAGATGTTAATAGACCAAGTGGCCGACCTCT	300
DB	241 AAAGGAGACCTGGAACCAACATCTCTTAAGATGTTAATAGACCAAGTGGCCGACCTCT	300
QY	301 TCATCTTATACATGATGAGAAAAAGAAATATTTCACGAAAAATCAGGACCATATGACTC	360
DB	301 TCATCTTATACATGATGAGAAAAAGAAATATTTCACGAAAAATCAGGACCATATGACTC	360
QY	361 CTGACCAAAAGAGAAAAAGTCAACAGACCTGAAGGAGAGAGACCGAGCTATTCTCTG	420
DB	361 CTGACCAAAAGAGAAAAAGTCAACAGACCTGAAGGAGAGAGACCGAGCTATTCTCTG	420
QY	421 GGAATGGGTATGATGATGTGTGCTCCATCATGATGTAATTTTCTGTGGGAATCAACTCTG	480
DB	421 GGAATGGGTATGATGATGTGTGCTCCATCATGATGTAATTTTCTGTGGGAATCAACTCTG	480
QY	481 CGCTCATCATGACAGAGCGTGTGAGCCAGAAAGTCAATGACCTTGCTGATACGCTC	540
DB	481 CGCTCATCATGACAGAGCGTGTGAGCCAGAAAGTCAATGACCTTGCTGATACGCTC	540
QY	541 ATCAGGGAACATTTAATCTGCTCCTTCACTGTGTGTCACGACTGTGAAAACTTTCTCAG	600
DB	541 ATCAGGGAACATTTAATCTGCTCCTTCACTGTGTGTCACGACTGTGAAAACTTTCTCAG	600
QY	601 TACCCCTGCTCCAGAGGTAGCTTAAGTGAATCTTCCGGGAAAAAAGCTCCTCCTCAG	660
DB	601 TACCCCTGCTCCAGAGGTAGCTTAAGTGAATCTTCCGGGAAAAAAGCTCCTCCTCAG	660
QY	661 CACACAGAAAGACATTAATAATCATAGAAAGTCTCCTATATACCTTAAATGTGAAAA	720
DB	661 CACACAGAAAGACATTAATAATCATAGAAAGTCTCCTATATACCTTAAATGTGAAAA	720
QY	721 AATTTGAAGATCCATGCTCCCTGGTGAATTTTGACAGAAAACTTCAGAAAGTATCA	780
DB	721 AATTTGAAGATCCATGCTCCCTGGTGAATTTTGACAGAAAACTTCAGAAAGTATCA	780
QY	781 CACTTCTCTGCTATTCTGACCCAGAAAGAAACAGAAAGTGTATCTTACCAAATC	840
DB	781 CACTTCTCTGCTATTCTGACCCAGAAAGAAACAGAAAGTGTATCTTACCAAATC	840
QY	841 TACAGTCCCAAGGCTGTTCATTTCACTCTTTGCGCAACCTGTATATGAGCTGGGGGT	900
DB	841 TACAGTCCCAAGGCTGTTCATTTCACTCTTTGCGCAACCTGTATATGAGCTGGGGGT	900
QY	901 GTGGCAATTGTTGCGATGTAATTTTCAACAGTACTCTCCCTCTATATGAGAGATC	960
DB	901 GTGGCAATTGTTGCGATGTAATTTTCAACAGTACTCTCCCTCTATATGAGAGATC	960
QY	961 CAAGGATCATATGATTAATGCAAAAAATGATTAATAATTTTGTAAAGCTCAATAC	1020

Dd		961	CACGGATCATAAGTAATGAAGCAAAATGATATAAAATATTGTGTTAAAGCTCAATAC	1020
Oy		1021	TGTTTCCTTTCATCTCCACCAAGAAGCTTAAGTTTGTAAGCGAGTCGTATAGT	1080
Dd		1021	TGTTTCCTTTCATCTCCACCAAGAAGCTTAAGTTTGTAAGCGAGTCGTATAGT	1080
Oy		1081	TCCTCATATATTTCTTATATATGTAGAGCAATATATGCAAAAGCTGTTCTATATGCACAATG	1140
Dd		1081	TCCTCATATATATTTCTTATATATGTAGAGCAATATATGCAAAAGCTGTTCTATATGCACAATG	1140
Oy		1141	ATGCTTATATATCTCAGAGAAATATATACCTGTTTGTTGTGA	1184
Dd		1141	ATGCTTATATATCTCAGAGAAATATATACCTGTTTGTTGTGA	1184
RESULT 2				
ID	AAZ51632	SEQUENCE	COMPARISON 'A'	
XX	AAZ51632 standard; cDNA; 1300 BP.			
XX	AAZ51632;			
XX	21-JUN-2000 (first entry)			
DE	Human membrane channel protein-16 (MECHP-16) cDNA.			
KV	Membrane channel protein-16; MECHP-16; diagnosis; treatment; lymphoma;			
KM	cell proliferative disorder; bursitis; arteriosclerosis; cancer; sarcoma;			
KW	inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;			
KV	diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;			
KM	muscular disorder; myocardiitis; Duchenne's muscular dystrophy; nocturnal;			
KV	cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac;			
KM	neurological disorder; Alzheimer's disease; Parkinson's disease; human;			
KV	Huntington's disease; antiarteriosclerotic; hepatotropic; cystostatic;			
KM	anti-HIV; antiaiemtic; neuroprotective; immunomodulator; antidiabetic;			
KV	hypertensive; vasoconstrictor; antiaslumatic; antiinflammatory; antidepressant;			
KM	anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.			
XX	Homo sapiens.			
OS				
XX				
Key	Location/Qualifiers			
FM	378..1085			
FT	/tag= a			
FT	/product= "MECHP-16"			
FT	/note= "Shows homology to human beta subunit of Ca+			
FT	activated K+ channel"			
FT	381..425			
FT	//tag= b			
FT	/bound_molecly= "Primer or Probe"			
XX				
FN	WC020012711-A2.			
FD				
XX	09-MAR-2000.			
XX				
XX	02-SEP-1999;	99NC-USO20468.		
FR	02-SEP-1998;	98US-0155226P.		
FR	12-NOV-1998;	98US-00191283.		
PR	09-DIC-1998;	98US-0155225P.		
PR	26-JAN-1999;	99US-0155211P.		
XX	10-FEB-1999;	99US-0155263P.		
XX	(INCY-) INCYTE PHARM INC.			
PI	An-Young J,	Bardman O, Tang YT, Reddy R, Hillman JT, Yue H;		
PI	Lai P, Corley NC, Gueglar KJ, Gorgone G, Baughn MR, Azimzai Y;			
XX	WP1: 2000-256643/22.			
DR	P-PBDB; AAY70466.			
PT	Novel human membrane channel protein and polynucleotide useful for			
PT	diagnosing and treating cell proliferative, inflammatory, secretory,			
PT	osmoregulatory, muscular, cardiovascular and neurological disorders.			

XX Claim 9: Page 128-129; 140pp; English.

PS The present sequence is a cDNA identified in Incyte clone 2069907 derived
 XX from ISLN001 cDNA library. It encodes human membrane channel protein-16
 CC (MECHP-16), which is expressed in nervous tissues. Anti-MECHP antibodies
 CC can be used as therapeutic antagonists and reagents for diagnosis and
 CC monitoring diseases. MECHP cDNA can be used for diagnosis of MECHP-
 CC related diseases and gene mapping. MECHP can be used for treatment of
 CC cell proliferative disorders such as psoriasis and atherosclerosis,
 CC cancers like lymphoma and sarcoma, inflammatory disorders like AIDS and
 CC Addison's disease, transport/secretory disorders like cystic fibrosis and
 CC diabetes mellitus, osmoregulatory disorders like diarrhoea and renal
 CC failure, muscular disorders like myocardiitis and Duchenne's muscular
 CC dystrophy, cardiovascular disorders like hypertension and vasculitis,
 CC congenital lung anomalies like bronchitis and asthma and neurological
 CC disorders like Alzheimer's disease, Parkinson's disease and Huntington's
 CC disease

XX Sequence 1300 BP; 381 A; 288 C; 279 G; 352 T; 0 U; 0 Other;

XX Query Match 99.6%; Score 1179.2; DB 3; Length 1300;
 XX Best Local Similarity 99.7%; Pred. No. 0;
 XX Matches 1181; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 CTTAATCTATCCAACTATGAGTACGCTCTGGTCTGTCTATGAGACCCAGGGGCAATG 60
 108 CTTAATCTATCCAACTATGAGTACGCTCTGGTCTGTCTATGAGACCCAGGGGCAATG 167
 61 TTGGAAAGAACTGAGAGAAAGCAAAAGCGGCGAGTGTGTAGAGGGGCAAGACGGG 120
 168 TTGGAAAGAACTGAGAGAAAGCAAAAGCGGCGAGTGTGTAGAGGGGCAAGACGGG 227
 121 CTGTGGGGGCGCTCCGAGAGAAATGTACTGAAAAGCTGACGCAATGCTGGGATTGGCTA 180
 228 CTGTGGGGGCGCTCCGAGAGAAATGTACTGAAAAGCTGACGCAATGCTGGGATTGGCTA 287
 181 AACAACTACTGGAAGCAGACAGGTTTTCCTCCATCTCTCCAGCAATCCACATAAG 240
 288 AACAACTACTGGAAGCAGACAGGTTTTCCTCCATCTCTCCAGCAATCCACATAAG 347
 241 AAGAGAGACCTGGAGCAACATCTCTAGATGTTTATGAGACAGAGCGGCGGACCTCT 300
 348 AAGAGAGACCTGGAGCAACATCTCTAGATGTTTATGAGACAGAGCGGCGGACCTCT 407
 301 TCATCTTATAGCATGATGAAAAAGAAATATTTCACGAAAAATCAGGAGCCATGACCTC 360
 408 TCATCTTATAGCATGATGAAAAAGAAATATTTCACGAAAAATCAGGAGCCATGACCTC 467
 361 CTGGACAAAAGAAAAAGCTACAGCACTGAAAGCGAGAGACCGAGCTATTCTCTG 420
 468 CTGGACAAAAGAAAAAGCTACAGCACTGAAAGCGAGAGACCGAGCTATTCTCTG 527
 421 GGAAGTGGATGATGATGATGCTCCATCATGATGATGATGATGATGATGATGATGATGAT 480
 528 GGAAGTGGATGATGATGATGCTCCATCATGATGATGATGATGATGATGATGATGATGAT 587
 481 CGCTCATACATGAGAGCGTGTGAGACGAGAGAGTCAATGACCTTGTGTAATGCTGTC 540
 588 CGCTCATACATGAGAGCGTGTGAGACGAGAGAGTCAATGACCTTGTGTAATGCTGTC 647
 541 ATCAGAGAAACATTTAATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 648 ATCAGAGAAACATTTAATGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
 601 TACCCCTGCTCCAGGTGTAGCTTAACTGACTTCTTCGCGGAAAAAGCTCTCTCTAC 660
 708 TACCCCTGCTCCAGGTGTAGCTTAACTGACTTCTTCGCGGAAAAAGCTCTCTCTAC 767
 661 CACACGAGAGAGAAATTAATTAATGATGAGAGTGTCTCTATATCTTAATGATGAGAAA 720
 768 CACACGAGAGAGAAATTAATTAATGATGAGAGTGTCTCTATATCTTAATGATGAGAAA 827

QY 721 AATTGAGAAATCCATGTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 828 AATTGAGAAATCCATGTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 887
 QY 781 CACTTCTCTGCTATTTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 888 CACTTCTCTGCTATTTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
 QY 841 TACGTTCCAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 948 TACGTTCCAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1007
 QY 901 GTGGCAATTTGTCAGATGAG 960
 DB 1008 GTGGCAATTTGTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1067
 QY 961 CAACGATCAATGATTAATGCAAAATGATTAATTAATTAATTAATTAATTAATTAATTA 1020
 DB 1068 CAACGATCAATGATTAATGCAAAATGATTAATTAATTAATTAATTAATTAATTAATTA 1127
 QY 1021 TGTTCCTTCATCTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1128 TGTTCCTTCATCTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1187
 QY 1081 TCCCTAATATTTCTTATATGATGAGCAATTAATGCAAAAGCTGTTCTATATGCAACATG 1140
 DB 1188 TCCCTAATATTTCTTATATGATGAGCAATTAATGCAAAAGCTGTTCTATATGCAACATG 1247
 QY 1141 ATGCTTATATTTCTGAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1184
 DB 1248 ATGCTTATATTTCTGAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1291

RESULT 3

ID AAA26355 standard; cDNA; 2098 BP.

AC AAA26355;

DT 29-JUN-2000 (first entry)

DE Human secreted protein gene 10 SEQ ID NO:20.

XX Human; secreted protein; diagnosis; cytosolic; immunosuppressive;
 KW antiHIV; antiinflammatory; neurotropic; neuroprotective; antiasthma;
 KW osteopathic; antiarthritic; antibacterial; antidiabetic; antidiabetic;
 KW antipruritic; cardiatic; gene therapy; cancer; neurological disorder;
 KW immune disease; inflammation; blood disorder; tumour; ss.

OS Homo sapiens.

PN W0200006698-A1.

PD 10-FEB-2000.

PE 29-JUL-1999; 99NO-US017130.

PR 30-JUL-1998; 98US-0094657P.

PR 05-AUG-1998; 98US-0095486P.

PR 06-AUG-1998; 98US-0095454P.

PR 12-AUG-1998; 98US-0096319P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Komatsu G.A., Rosen C.A., Ruben S.M., Duan R., Moore P.A., Shi Y.

PI Lefleur D., Wei Y., Ni J., Florence K.A., Young P.E., Brewer L.A.

PI Sogner D.R., Endress G.A., Ebner R., Olsen H.S., Mucenski M.

DR WPI, 2000-195282/17.

DR P-PSDB; AA91460.

New isolated human genes and the secreted polypeptides they encode,